

TABLE S2 Antibiotic resistance determinants found in *C. gilardii* W2-2 with a strong^a match in the CARD database.

Locus tag (GenBank)	Predicted protein in <i>C. gilardii</i> W2-2 (PATRIC annotation)	Closest match in CARD database ^b				% Identity to W2-2 ^c	
		Closest match in CARD database	% Identity	% Similarity	% Coverage	CR3	JZ4
FX016_22760 (MN313 890)	Class D beta-lactamase OXA-837 (EC 3.5.2.6)	<i>Ralstonia picketti</i> OXA-60 β-lactamase <i>P. aeruginosa</i> OXA-50 β-lactamase	49 50	65 65	84 77	83	82
FX016_08315 (MN366 378)	Aminoglycoside 3-N-acetyltransferase [AAC(3)-IVb / AacC10] (EC 2.3.1.81)	<i>Escherichia coli</i> and <i>Pseudomonas stutzeri</i> AAC(3)-IVa	73	83	99	83	83
FX016_04685 (MN366 379)	Aminoglycoside 3"-adenylyltransferase [ANT(3")-Ib / AadA32] (EC 2.7.7.47)	<i>E. coli</i> aminoglycoside-(3")(9)-adenylyltransferase AadA16 <i>Pseudomonas aeruginosa</i> streptomycin 3"-adenylyltransferase AadA11	41 40	59 57	87 85	Absent	78
FX016_17790	Multidrug efflux system EmrAB-OMF, inner-membrane proton/drug antiporter EmrB (MFS type)	EmrB component of <i>E. coli</i> EmrAB-TolC pump	55	71	93	98	95
FX016_17785	Multidrug efflux system EmrAB-OMF, membrane fusion component EmrA	EmrA component of <i>E. coli</i> EmrAB-TolC pump	47	64	91	99	95
FX016_17780	Outer membrane factor (OMF) lipoprotein associated with EmrAB-OMF efflux system	AdeH component of <i>Acinetobacter baumannii</i> AdeFGH pump	35	54	80	96	95
FX016_05295	Multidrug efflux system MdtABC-TolC, inner-membrane proton/drug antiporter MdtB (RND type)	MdtB component of <i>E. coli</i> MdtABC-TolC pump MuxB component of <i>P. aeruginosa</i> MuxABC-OpmB pump	68 72	82 84	97 98	99	99
FX016_05290	Multidrug efflux system MdtABC-TolC, inner-membrane proton/drug antiporter MdtC (RND type)	MdtC component of <i>E. coli</i> MdtABC-TolC pump MuxC component of <i>P. aeruginosa</i> MuxABC-OpmB pump	60 59	74 73	98 99	98	99

FX016_05300	Multidrug efflux system MdtABC-TolC, membrane fusion component MdtA	MdtA component of <i>E. coli</i> MdtABC-TolC pump MuxA component of <i>P. aeruginosa</i> MuxABC-OpmB pump	46 53	63 71	73 62	96	97
FX016_05285	Outer membrane factor (OMF) lipoprotein associated with MdtABC efflux system	OpmB component of <i>P. aeruginosa</i> MuxABC-OpmB pump	53	67	91	94	89
FX016_08510	RND efflux system, inner membrane transporter	AcrB component of <i>E. coli</i> AcrAB-TolC pump	61	77	97	99	99
FX016_08515	RND efflux system, membrane fusion protein	AcrA component of <i>E. coli</i> AcrAB-TolC pump	49	67	94	97	97
FX016_08505	Efflux transport system, outer membrane factor (OMF) lipoprotein	OprM component of <i>P. aeruginosa</i> MexAB-OprM and other pumps	49	67	96	96	96
FX016_02620	RND efflux system, inner membrane transporter	MexB component of <i>P. aeruginosa</i> MexAB-OprM pump	79	89	99	97 ^d	97
FX016_02625	Multidrug efflux system, membrane fusion component MexA of MexAB-OprM	MexA component of <i>P. aeruginosa</i> MexAB-OprM pump	65	82	98	95 ^d	95
FX016_00070	Multidrug efflux system, inner membrane proton/drug antiporter (RND type) MexD of MexCD-OprJ system	MexD component of <i>P. aeruginosa</i> MexCD-OprJ pump	67	79	98	90	92
FX016_00075	Multidrug efflux system, membrane fusion component MexC of MexCD-OprJ system	MexC component of <i>P. aeruginosa</i> MexCD-OprJ pump	62	75	92	97	97
FX016_00065	Efflux transport system, outer membrane factor (OMF) lipoprotein	OprJ component of <i>P. aeruginosa</i> MexCD-OprJ pump	60	71	91	91	92
FX016_03005	RND efflux system, inner membrane transporter	AdeF component of <i>Acinetobacter baumannii</i> AdeFGH pump	76	86	99	99	98
FX016_03010	RND efflux system, membrane fusion protein	AdeG component of <i>Acinetobacter baumannii</i> AdeFGH pump	55	73	88	98	98
FX016_03000	Efflux transport system, outer membrane factor (OMF) lipoprotein	AdeH component of <i>Acinetobacter baumannii</i> AdeFGH pump	51	68	93	98	98
FX016_08590	RND efflux system, inner membrane transporter	MuxB component of <i>P. aeruginosa</i> MuxABC-OpmB pump	47	66	98	98	98

FX016_08595	RND efflux system, membrane fusion protein	MuxA component of <i>P. aeruginosa</i> MuxABC-OpmB pump	36	55	92	98	98
FX016_08585	Hypothetical protein	MdsC component of <i>Salmonella enterica</i> MdsABC pump	30	49	24	85	90
FX016_13945	RND efflux system, inner membrane transporter	MdsB component of <i>Salmonella enterica</i> MdsABC pump MexF component of <i>P. aeruginosa</i> MexEF-OprN pump	46	65	99	40	95
FX016_13950	RND efflux system, membrane fusion protein	MdsA component of <i>S. enterica</i> MdsABC pump MexE component of <i>P. aeruginosa</i> MexEF-OprN pump	38	57	77	36	87
FX016_13940	Efflux transport system, outer membrane factor (OMF) lipoprotein	OprN component of <i>P. aeruginosa</i> MeEF-OprN pump OpmD component of <i>P. aeruginosa</i> MexGHI-OpmD pump	31	48	92	34	87
FX016_16430	RND efflux system, inner membrane transporter	MexK component of <i>P. aeruginosa</i> MexJK-OprM/H pump	54	70	99	99	99
FX016_16435	CzcABC family efflux RND transporter, membrane fusion protein	MexJ component of <i>P. aeruginosa</i> MexJK-OprM/H pump	40	56	71	93	95
FX016_08485	Fosmidomycin resistance protein	RosA component of <i>Yersinia enterocolitica</i> RosAB pump	60	75	96	95	98

^aTable S2 includes the 30 predicted proteins from *C. gilardii* W2-2 found to have a strong match in the CARD database. We identified these predicted proteins by analyzing all 40 genes initially mapped to the CARD or PATRIC AMR databases (See Material and Methods in the manuscript for full details), as well as all other genes annotated as potential antibiotic resistance genes or drug efflux transporters. In general, predicted proteins were considered to have a strong match in the CARD database when they had greater than 65% similarity and 80% coverage to one or more antibiotic resistance proteins in the CARD database. Despite being below the aforementioned threshold, we also included ANT(3")-Ib (AadA32), because of its annotation as a aminoglycoside 3"-adenylyltransferase, and because it decreased susceptibility to

spectinomycin and streptomycin when cloned in *E. coli* (see Table 4 in the manuscript). For multicomponent efflux pumps that appear to be encoded by genes in the same operon, all components found in *C. gilardii* W2-2 are shown in the table if at least one of them met the aforementioned threshold. Predicted proteins are designated using their PATRIC annotation, which provides more information regarding protein function; however, the corresponding GenBank locus tag identifier is also provided. For the first 3 proteins in the table, which were cloned and their effect on antibiotic susceptibility tested (Tables 4 and 5), their official annotation is used and both their locus tag identifier in the genome, as well as their individual accession number (shown in parenthesis), are provided.

^bClosest CARD match for the predicted protein in *C. gilardii* W2-2. The percent (%) identity, similarity and coverage between the predicted protein of *C. gilardii* W2-2 its closest CARD match are also shown.

^cPercent identity between the predicted protein of *C. gilardii* W2-2 and the predicted proteins of *C. gilardii* CR3 or JZ4 strains.

^dMexA and MexB in *C. gilardii* CR3 are annotated together as a single predicted protein labeled MexB.

Table S2 footnote, continued.